

Modeling Strategies for Containing Pandemic Influenza in the U.S.

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The avian influenza H5N1 strain has recently spread among poultry from Southeast Asia and Russia to Europe, probably by migrating birds. So far humans can only be infected by poultry, which makes it a slow spreading disease in humans. However death rates of about 50% are extremely high so far for the about 100 infected humans. By mutation or reassortment with a human strain of influenza, H5N1 influenza could become human-to-human transmissible and cause a worldwide pandemic like the 1918 Spanish flu, or the 1957 and 1968 pandemics which killed tens of millions of people worldwide.

What can be done if such a pandemic hits the world? The current flu shots distributed each year will not protect people from this aggressive strain, never before seen by human immune systems. A variety of mitigation strategies and their combinations have to be imposed by the government. In addition to vaccines and therapeutics, these include the reduction of travel, school closure, nonessential work closure, and other social distancing measures, up to a mandatory quarantine. There are medical opportunities like antiviral drugs that can help prevent transmission of the virus, however this medication (known as the product name Tamiflu) is expensive and in short supply, and thus should be carefully distributed to get the most efficiency per dose. Another opportunity is the fast development of a vaccine, possibly with a low efficacy due to fast production.

In order to test these mitigation strategies and to optimize their combinations, we have developed an agent-based model for the U.S. that captures the transmission of the virus in different mixing groups like community, workplaces, household clusters, schools, and households. In this large-scale model the 280 million agents are distributed among five age groups according to demographic data. This underlying community structure is similar to previous small-scale models [1–3]. The geographic distribution is represented by about 60,000 tracts (each containing about 5000 people) and movement of people between the tracts, whereby the movement is given by data from the transportation bureau and can be split into daily commuter travel to work and longer distance travel (business trips, vacation, etc.). By fitting the model parameters to different aggressive strains — as represented by the basic reproductive number R_0 (basically the number of persons a sick individual infects directly) — of the hypothetical virus, several mitigation scenarios for different virus strengths could be investigated. Preliminary results suggest that for reproductive numbers R_0 less than 2.0, targeted administration of antiviral drugs helps control the spread until vaccine is developed. For more aggressive viruses a more sophisticated combination of measures is necessary to control the spread.

It is noteworthy that the simulations were run on large multiprocessor machines and that we used our large-scale MD platform SPaSM [4] as a base for the multimillion agent simulations necessary for this work. For example, a typical run for one flu season takes about 12 hours on 256 CPUs of the Pink system at Los Alamos. This work was featured in a recent Scientific American article [5].

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- [1] M.E. Halloran, et al., *Science* **298**, 1428 (2002).
- [2] I.M. Longini, *Am. J. Epidemiol.* **159**, 623 (2004).
- [3] I.M. Longini et al., *Science* **309**, 1083 (2005).
- [4] D.M. Beazley and P. S. Lomdahl, *Parallel Comput.* **20**, 173 (1994).
- [5] W.W. Gibbs and C. Soares, *Scientific American* **293** (5), 44 (2005).

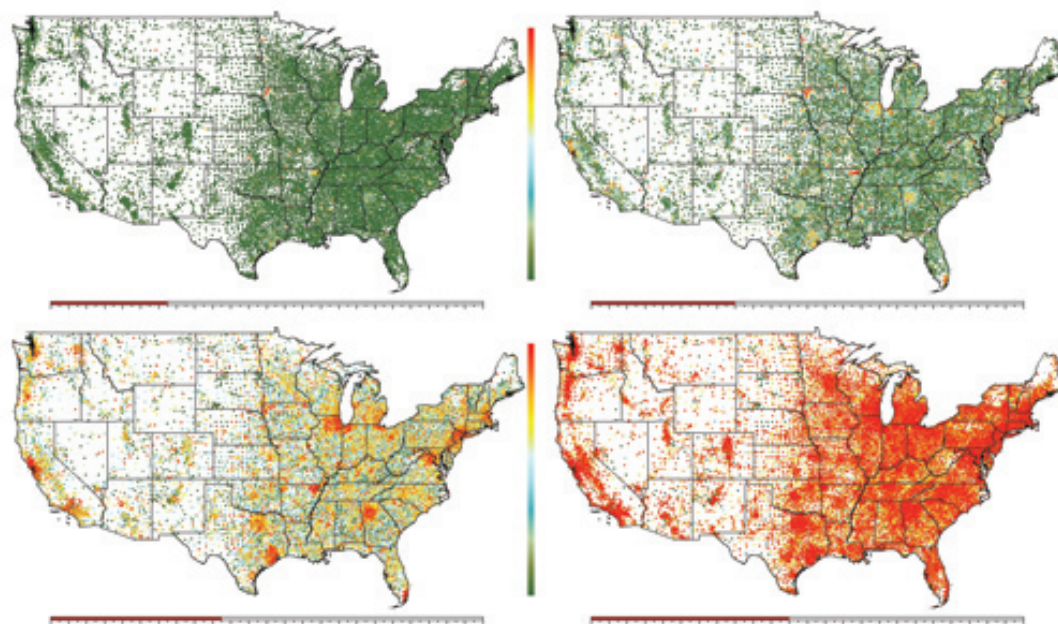


Fig. 1. Baseline simulation realization of a pandemic flu outbreak with $R_0 = 1.6$, introduced by the daily entry of a number of infected individuals through 14 major international airports in the continental U.S. (beginning on day 0). The spatiotemporal dynamics of the prevalence (number of symptomatic cases at any point in time) is indicated on a logarithmic color scale at the right edge of each figure, from 0.3–30 cases per 1,000 residents. Snapshots are shown at (left to right, top to bottom) day 65, 80, 95, 110. Each dot on the map represents a tract containing on average of 5000 people; therefore the density of the dots indicates the population density.